Identifying sources of mutation in human induced pluripotent stem cells by whole genome sequencing

Grant Award Details

Identifying sources of mutation in human induced pluripotent stem cells by whole genome sequencing

Grant Type: Basic Biology III

Grant Number: RB3-02186

Project Objective: Goal is to identify mutations in human iPSC lines and determine their likely origin, eg. reprogramming methodology vs. culture and expansion conditions, somatic cell origins, etc.

Investigator:

Name:	Kristin Baldwin
Institution:	Scripps Research Institute
Type:	PI

Human Stem Cell Use: iPS Cell

Award Value: $1,705,500

Status: Closed

Progress Reports

Reporting Period: Year 1

View Report

Reporting Period: Year 2

View Report

Reporting Period: Year 3

View Report

Grant Application Details

Application Title: Identifying sources of mutation in human induced pluripotent stem cells by whole genome sequencing

Public Abstract: Stem cell research offers new tools to help treat and cure diseases that affect diverse cells types in the body such as neurological diseases, heart disease and diabetes by producing human cells for transplantation or to enable drug discovery . Recent advances have allowed researchers to generate patient-matched cell types from the skin or other tissues of patients. These patient-matched cells are important because they are unlikely to cause immune rejection upon transplantation and they may help to model diseases caused by gene variations found only in rare individuals. Despite their promise, patient-matched cells differ from traditional stem cells in ways that may cause them to be less stable or increase their potential to cause tumors. This is because patient-matched cells are generated from tissues taken from adult patients using methods that dramatically alter the chromosomes of these cells. These factors could endow these reprogrammed cells with mutations that would not be present in cells derived from embryonic sources. To ensure the safety and clinical utility of reprogrammed cells, it is critical to establish methods to identify potentially oncogenic or detrimental mutations. This proposal is designed to identify the source and scope of mutations in reprogrammed pluripotent cell lines using cutting edge whole genome sequencing methods. Results of these studies will establish the relative safety of current methods to produce patient-matched reprogrammed cells and help to improve methods to speed the translation of these advances into therapies.

Statement of Benefit to California: California has become an epicenter of stem cell advancement in part due to the funding of innovative collaborative research by the CIRM. We have established new methods that will improve the safety and effectiveness of regenerative medicine in cases where cell therapies are generated by converting adult cells into other cell types, including pluripotent cells and differentiated cells such as neurons and heart cells. This will help to reduce the costs of ongoing research funded by CIRM and by other California entities. Results of these studies will help to accelerate the translational application of basic biomedical advances being achieved across the state.
